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RAW SEQUENCE LISTING

DATE: 04/09/2002

PATENT APPLICATION: US/09/768,155

TIME: 11:26:25

Input Set : N:\Crif3\RULE60\09768155.raw

Output Set: N:\CRF3\04092002\I768155.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

- 4 (i) APPLICANT: Morris Reichlin and Eugen Koren
 5 (ii) TITLE OF INVENTION: METHOD FOR TREATMENT OF SLE
 7 (iii) NUMBER OF SEQUENCES: 12
 9 (iv) CORRESPONDENCE ADDRESS:

- 10 (A) ADDRESSEE: Patrea L. Pabst
 11 (B) STREET: 2800 One Atlantic Center
 12 1201 West Peachtree Street
 13 (C) CITY: Atlanta
 14 (D) STATE: Georgia
 15 (E) COUNTRY: USA
 16 (F) ZIP: 30306-3450

18 (v) COMPUTER READABLE FORM:

- 19 (A) MEDIUM TYPE: Floppy disk
 20 (B) COMPUTER: IBM PC compatible
 21 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 22 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

24 (vi) CURRENT APPLICATION DATA:

- C--> 25 (A) APPLICATION NUMBER: US/09/768,155
 C--> 26 (B) FILING DATE: 23-Jan-2001
 32 (C) CLASSIFICATION:

29 (vii) PRIOR APPLICATION DATA:

- 30 (A) APPLICATION NUMBER: 08/800,682
 31 (B) FILING DATE:

34 (viii) ATTORNEY/AGENT INFORMATION:

- 35 (A) NAME: Pabst, Patrea L.
 36 (B) REGISTRATION NUMBER: 31,284
 37 (C) REFERENCE/DOCKET NUMBER: OMRP 158 CIP

39 (ix) TELECOMMUNICATION INFORMATION:

- 40 (A) TELEPHONE: (404)873-8794
 41 (B) TELEFAX: (404)873-8795

43 (2) INFORMATION FOR SEQ ID NO: 1:

44 (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1314 base pairs
 46 (B) TYPE: nucleic acid
 47 (C) STRANDEDNESS: single
 48 (D) TOPOLOGY: linear

W--> 49 (ii) MOLECULE TYPE: DNA

50 (iii) HYPOTHETICAL: NO

51 (iv) ANTI-SENSE: NO

52 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

54 GGTGAAGAAG GAGTTGTGCC AGCACGTGAG TACTCAGACG ATCGTAACAT CAACCTGGCA 60

ENTERED

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56 GACGAATTAA AAATTGGTGA TACCATTGAA GCAGTTGTCA TTTCTAACGT AACAAGCGAC 120
58 AAGGAAGGCG TCAGTTACTT GTTGTCAAAG AAGCGTTTGG ATGCGCGCAA GGCATGGGAA 180
60 AACTTGAGCT TTGCTGAAGG TGACACAGTT GATGCCAAGG TTATCAACGC TGTTCGTGGT 240
62 GGTTCGATTG TTGATGTTAA CGGCGTACGT GGTTCGTAC CAGCATCAAT GGTTGCAGAA 300
64 CGTTTCGTTT CTGATTTGAA CCAATTCAAG AATAAGGATA TTAAAGCACA AGTTATCGAA 360
66 ATTGACCCTG CTAATGCACG TTTGATTTTG TCACGTAAGG CTGTTGCTGC ACAAGAACGC 420
68 GCTGCACGAT TGGCTGAAGT ATTTAGCAAG TTGTCAGTTC GTGAAGTTGT TGAAGGAACT 480
70 GTTGCCCGTT TGACAGACTT CGGCGCATTG GTTGACTTGG GTGGTGTGA TGGTTTGGTT 540
72 CACGTATCAG AAATCTCACA CGATCGTGTG AAGAACCCGG CCGATGTATT GACAAAGGGT 600
74 GACAAGGTTG ATGTTAAGAT CTTGGCATTG GACACTGAAA AGGGTCGTAT CTCATTGTCA 660
76 ATCAAAGCAA CACAACGTGG ACCTTGGGAC GAAGCTGCAG ATCAAATCGC TGCAGGTTCA 720
78 GTGCTTGAAG GTACTGTTAA GCGTGTGAAG GACTTTGGTG CCTTTGTTGA AATTTTGCCT 780
80 GGTATCGAAG GTCTTGTGCA CGTGTCACAA ATTTCAAACA AGCGTATTGA AAACCCATCA 840
82 GAAGTTTGA AGTCTGGTGA CAAGGTACAA GTGAAGGTAT TGGACATTAA GCCAGCCGAA 900
84 GAACGTATTT CATTGTCAAT GAAGGCTTTG GAAGAAAAGC CAGAACGTGA AGATCGTCGT 960
86 GGTAACGATG GTTCAGCTTC ACGTGCTGAT ATCGCTGCTT ACAAGCAACA AGATGACTCA 1020
88 GCCGCAACAT TGGGTGACAT CTTTGGTGAT AAGTTGTAAG AGGCATCAAC ATAAAAGAGC 1080
90 TGGTTCGCCA GTTCTTTTAT TTTTGAAGAA AAATTGAGTG GGCATTAGTG GCGGCTCACG 1140
92 GTATGAAAAA GGAGGTGCGA TTATGGCAGC ACCAGTAGTA GCCATTGTTG GCGACCAAAC 1200
94 GTCGGAAAAT CGACTATCTT TAACCGGATG GCCGGAGAAC GTATTGCAAT TGTGAAGAT 1260
96 CAACCAGGGG TAACACGCGA TCGTTGTAC GCGCCAGCCG AATGGTTGAA TTAT 1314

```

98 (2) INFORMATION FOR SEQ ID NO: 2:

99 (i) SEQUENCE CHARACTERISTICS:

100 (A) LENGTH: 352 amino acids

101 (B) TYPE: amino acid

102 (C) STRANDEDNESS: single

103 (D) TOPOLOGY: linear

104 (ii) MOLECULE TYPE: protein

105 (iii) HYPOTHETICAL: NO

106 (iv) ANTI-SENSE: NO

107 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

109 Gly Glu Glu Gly Val Val Pro Ala Arg Glu Tyr Ser Asp Asp Arg Asn
110 1 5 10 15
112 Ile Asn Leu Ala Asp Glu Leu Lys Ile Gly Asp Thr Ile Glu Ala Val
113 20 25 30
115 Val Ile Ser Asn Val Thr Ser Asp Lys Glu Gly Val Ser Tyr Leu Leu
116 35 40 45
118 Ser Lys Lys Arg Leu Asp Ala Arg Lys Ala Trp Glu Asn Leu Ser Phe
119 50 55 60
121 Ala Glu Gly Asp Thr Val Asp Ala Lys Val Ile Asn Ala Val Arg Gly
122 65 70 75 80
124 Gly Leu Ile Val Asp Val Asn Gly Val Arg Gly Phe Val Pro Ala Ser
125 85 90 95
127 Met Val Ala Glu Arg Phe Val Ser Asp Leu Asn Gln Phe Lys Asn Lys
128 100 105 110
130 Asp Ile Lys Ala Gln Val Ile Glu Ile Asp Pro Ala Asn Ala Arg Leu
131 115 120 125
133 Ile Leu Ser Arg Lys Ala Val Ala Ala Gln Glu Arg Ala Ala Gln Leu
134 130 135 140

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```

136 Ala Glu Val Phe Ser Lys Leu Ser Val Gly Glu Val Val Glu Gly Thr
137 145          150          155          160
139 Val Ala Arg Leu Thr Asp Phe Gly Ala Phe Val Asp Leu Gly Gly Val
140          165          170          175
142 Asp Gly Leu Val His Val Ser Glu Ile Ser His Asp Arg Val Lys Asn
143          180          185          190
145 Pro Ala Asp Val Leu Thr Lys Gly Asp Lys Val Asp Val Lys Ile Leu
146          195          200          205
148 Ala Leu Asp Thr Glu Lys Gly Arg Ile Ser Leu Ser Ile Lys Ala Thr
149          210          215          220
151 Gln Arg Gly Pro Trp Asp Glu Ala Ala Asp Gln Ile Ala Ala Gly Ser
152 225          230          235          240
154 Val Leu Glu Gly Thr Val Lys Arg Val Lys Asp Phe Gly Ala Phe Val
155          245          250          255
157 Glu Ile Leu Pro Gly Ile Glu Gly Leu Val His Val Ser Gln Ile Ser
158          260          265          270
160 Asn Lys Arg Ile Glu Asn Pro Ser Glu Val Leu Lys Ser Gly Asp Lys
161          275          280          285
163 Val Gln Val Lys Val Leu Asp Ile Lys Pro Ala Glu Arg Ile Ser
164          290          295          300
166 Leu Ser Met Lys Ala Leu Glu Glu Lys Pro Glu Arg Glu Asp Arg Arg
167 305          310          315          320
169 Gly Asn Asp Gly Ser Ala Ser Arg Ala Asp Ile Ala Ala Tyr Lys Gln
170          325          330          335
172 Gln Asp Asp Ser Ala Ala Thr Leu Gly Asp Ile Phe Gly Asp Lys Leu
173          340          345          350

```

175 (2) INFORMATION FOR SEQ ID NO: 3:

176 (i) SEQUENCE CHARACTERISTICS:

177 (A) LENGTH: 255 amino acids

178 (B) TYPE: amino acid

179 (C) STRANDEDNESS: single

180 (D) TOPOLOGY: linear

181 (ii) MOLECULE TYPE: protein

182 (iii) HYPOTHETICAL: NO

183 (iv) ANTI-SENSE: NO

184 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

186 Ser Phe Ala Glu Gly Asp Thr Val Asp Ala Lys Val Ile Asn Ala Val
187 1          5          10          15
189 Arg Gly Gly Leu Ile Val Asp Val Asn Gly Val Arg Gly Phe Val Pro
190          20          25          30
192 Ala Ser Met Val Ala Glu Arg Phe Val Ser Asp Leu Asn Gln Phe Lys
193          35          40          45
195 Asn Lys Asp Ile Lys Ala Gln Val Ile Glu Ile Asp Pro Ala Asn Ala
196          50          55          60
198 Arg Leu Ile Leu Ser Arg Lys Ala Val Ala Ala Gln Glu Arg Ala Ala
199 65          70          75          80
201 Gln Leu Ala Glu Val Phe Ser Lys Leu Ser Val Gly Glu Val Val Glu
202          85          90          95
204 Gly Thr Val Ala Arg Leu Thr Asp Phe Gly Ala Phe Val Asp Leu Gly

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Output Set: N:\CRF3\04092002\I768155.raw

```

205          100          105          110
207 Gly Val Asp Gly Leu Val His Val Ser Glu Ile Ser His Asp Arg Val
208          115          120          125
210 Lys Asn Pro Ala Asp Val Leu Thr Lys Gly Asp Lys Val Asp Val Lys
211          130          135          140
213 Ile Leu Ala Leu Asp Thr Glu Lys Gly Arg Ile Ser Leu Ser Ile Lys
214 145          150          155          160
216 Ala Thr Gln Arg Gly Pro Trp Asp Glu Ala Ala Asp Gln Ile Ala Ala
217          165          170          175
219 Gly Ser Val Leu Glu Gly Thr Val Lys Arg Val Lys Asp Phe Gly Ala
220          180          185          190
222 Phe Val Glu Ile Leu Pro Gly Ile Glu Gly Leu Val His Val Ser Gln
223          195          200          205
225 Ile Ser Asn Lys Arg Ile Glu Asn Pro Ser Glu Val Leu Lys Ser Gly
226          210          215          220
228 Asp Lys Val Gln Val Lys Val Leu Asp Ile Lys Pro Ala Glu Glu Arg
229 225          230          235          240
231 Ile Ser Leu Ser Met Lys Ala Leu Glu Glu Lys Pro Glu Arg Glu
232          245          250          255
234 (2) INFORMATION FOR SEQ ID NO: 4:
235 (i) SEQUENCE CHARACTERISTICS:
236 (A) LENGTH: 254 amino acids
237 (B) TYPE: amino acid
238 (C) STRANDEDNESS: single
239 (D) TOPOLOGY: linear
240 (ii) MOLECULE TYPE: protein
241 (iii) HYPOTHETICAL: NO
242 (iv) ANTI-SENSE: NO
243 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
245 Ala Tyr Glu Asp Ala Glu Thr Val Thr Gly Val Ile Asn Gly Lys Val
246 1          5          10          15
248 Lys Gly Gly Phe Thr Val Glu Leu Asp Gly Ile Arg Ala Phe Leu Pro
249          20          25          30
251 Gly Ser Leu Val Asp Val Arg Pro Val Arg Asp Thr Leu His Leu Glu
252          35          40          45
254 Gly Lys Glu Leu Glu Phe Lys Val Ile Lys Leu Asp Gln Lys Arg Asn
255          50          55          60
257 Asn Val Val Val Ser Arg Arg Ala Val Ile Glu Ser Glu Asn Ser Ala
258 65          70          75          80
260 Glu Arg Asp Gln Leu Leu Glu Asn Leu Gln Glu Gly Met Glu Val Lys
261          85          90          95
263 Gly Ile Val Lys Asn Leu Thr Asp Tyr Gly Ala Phe Val Asp Leu Gly
264          100          105          110
266 Gly Val Asp Gly Leu Leu His Ile Thr Asp Met Ala Trp Lys Arg Val
267          115          120          125
269 Lys His Pro Ser Glu Ile Val Asn Val Gly Asp Glu Ile Thr Val Lys
270          130          135          140
272 Val Leu Lys Phe Asp Arg Glu Arg Thr Arg Val Ser Leu Gly Leu Lys
273 145          150          155          160

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```

275 Gln Leu Gly Glu Asp Pro Trp Val Ala Ile Ala Lys Arg Tyr Pro Glu
276          165          170          175
278 Gly Thr Lys Leu Thr Gly Arg Val Thr Asn Leu Thr Asp Tyr Gly Cys
279          180          185          190
281 Phe Val Glu Ile Glu Glu Gly Val Glu Gly Leu Val His Val Ser Glu
282          195          200          205
284 Met Arg Asp Arg Val Glu Asp Ala Thr Leu Val Leu Ser Val Gly Asp
285          210          215          220
287 Glu Val Glu Ala Lys Phe Thr Gly Val Asp Arg Lys Asn Arg Ala Ile
288 225          230          235          240
290 Ser Leu Ser Val Arg Ala Lys Asp Glu Ala Asp Glu Lys Asp
291          245          250
294 (2) INFORMATION FOR SEQ ID NO: 5:
295     (i) SEQUENCE CHARACTERISTICS:
296         (A) LENGTH: 247 amino acids
297         (B) TYPE: amino acid
298         (C) STRANDEDNESS: single
299         (D) TOPOLOGY: linear
300     (ii) MOLECULE TYPE: protein
301     (iii) HYPOTHETICAL: NO
302     (iv) ANTI-SENSE: NO
303     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
305 Lys Phe Glu Ala Gly Glu Arg Val Glu Gly Ile Ile Phe Asn Gln Val
306 1          5          10          15
308 Lys Gly Gly Phe Thr Val Asp Leu Asp Gly Ala Val Ala Phe Leu Pro
309          20          25          30
311 Arg Ser Gln Val Asp Ile Arg Pro Ile Arg Asp Val Thr Pro Ala Asp
312          35          40          45
314 Ala Gln Pro Ala Ala Leu Arg Asn Leu Lys Met Asp Lys Arg Arg Gly
315          50          55          60
318 Asn Ile Val Val Ser Arg Arg Thr Val Leu Glu Ser Arg Ala Glu
319 65          70          75          80
321 Gln Arg Ser Glu Ile Val Gln Asn Leu Glu Gly Gln Val Val Glu
322          85          90          95
324 Gly Val Val Lys Asn Ile Thr Asp Tyr Gly Ala Phe Val Asp Leu Gly
325          100         105         110
327 Gly Ile Asp Gly Leu Leu His Val Thr Asp Met Ala Trp Arg Arg Val
328          115         120         125
330 Lys His Pro Ser Glu Ile Gln Asn Ile Gly Gln Gln Val Lys Val Gln
331          130         135         140
333 Ile Ile Arg Ile Asn Gln Glu Thr His Arg Ile Ser Leu Gly Met Lys
334 145         150         155         160
336 Gln Leu Glu Ser Asp Pro Trp Asp Gly Ile Gly Ala Lys Tyr Pro Val
337          165         170         175
339 Gly Lys Lys Ile Ser Gly Thr Val Thr Asn Ile Thr Asp Tyr Gly Ala
340          180         185         190
342 Phe Val Glu Leu Glu Pro Gly Ile Glu Gly Leu Ile His Ile Ser Glu
343          195         200         205
346 Met Asn Arg Pro Gly Glu Gln Val Ile Glu Glu Phe Asn Lys Gly Asp

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VERIFICATION SUMMARY

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TIME: 11:26:26

Input Set : N:\Crf3\RULE60\09768155.raw

Output Set: N:\CRF3\04092002\I768155.raw

L:25 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:26 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:49 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1